This listing of claims will replace all prior versions, and listings, of claims in the application:

18. (Withdrawn) An isolated and purified nucleic acid sequence capable of hybridizing to a region of the long arm of chromosome 9 between D9S127 and D9S59, wherein said sequence is sufficiently linked to the familial dysautonomia gene to diagnose familial dysautonomia with the proviso that the nucleic acid sequence is not a sequence selected from the group consisting of D9S58 and D9S59.

19. (Withdrawn) An isolated and purified nucleic acid sequence capable of hybridizing to a region of the long arm of chromosome 9 between D9S53 and D9S105, wherein said sequence is sufficiently linked to the familial dysautonomia gene to diagnose familial dysautonomia with the proviso that the nucleic acid sequence is not a sequence selected from the group consisting of D9S58 and D9S59.

20. (Previously presented) A method for detecting the presence in a subject of a polymorphism linked to a gene associated with familial dysautonomia which comprises:

analyzing human chromosome 9 of the subject and detecting the presence of a polymorphism located between D9S59 and D9S127 inclusive and linked to the gene associated with familial dysautonomia and wherein the presence of the polymorphism is indicative of carriers of a gene associated with familial dysautonomia.

21. (Previously presented) The method according to claim 20, wherein the polymorphism is located on the q31 band of the long arm of human chromosome 9.

22. (Previously presented) The method according to claim 20, wherein the polymorphism is located about 20 cM around D9S309.

23. (Previously presented) The method according to claim 22, wherein the polymorphism is located about 10 cM around D9S309.

24. (Previously presented) The method according to claim 20, wherein the polymorphism is located about 20 cM around D9S310.

25. (Previously presented) The method according to claim 24, wherein the polymorphism is located about 10 cM around D9S310.

26. (Previously presented) The method according to claim 20, wherein the analyzing is carried out by:

(a) amplifying the polymorphism;

(b) separating the amplified polymorphism to generate a polymorphism pattern;

(c) correlating the presence or absence of the polymorphism with the respective presence or absence of the gene associated with familial dysautonomia by comparing a corresponding polymorphism pattern for family members showing segregation between the familial dysautonomia gene and the polymorphism,

27. (Previously presented) The method according to claim 26, wherein the polymorphism is detected by autoradiography.

28. (Previously presented) The method according to claim 26, wherein the polymorphism pattern of the subject is compared to the corresponding polymorphism pattern for each parent of the subject which are unaffected by familial dysautonomia disease and a family member affected by familial dysautonomia disease.

29. (Previously presented) A method for detecting the presence of polymorphisms linked to a gene associated with familial dysautonomia in a subject, comprising:

(a) detecting a maternal polymorphism linked to the gene associates with familial dysautonomia;

(b) detecting a paternal polymorphism linked to the gene associated with familial dysautonomia;

(c) typing the subject to determine the maternal polymorphism and paternal polymorphism;

(d) linking the distribution of the maternal polymorphism and paternal polymorphism with familial dysautonomia; and

(e) determining if the subject has the polymorphism located on the long arm of human chromosome 9 between D9S59 and D9S127, inclusive, linked to a gene associated with familial dysautonomia.

30. (Previously presented) A method for detecting the presence of polymorphisms linked to a gene associated with familial dysautonomia in a subject comprising typing blood relatives of a subject for a polymorphism located on the long arm of human chromosome 9 located between D9S59 and D9S127, inclusive, and linked to the gene associated with familial dysautonomia; and analyzing DNA from the subject and detecting the presence of the polymorphism linked to the gene associated with familial dysautonomia.

31. (Previously presented) The method according to claim 30, wherein the polymorphism is located within 10 cM of D9S309.

32. (Previously presented) The method according to claim 30, wherein the polymorphism is located within 10 cM of D9S310.

33. (New) The method according to claim 20 wherein the polymorphism is D9S59.